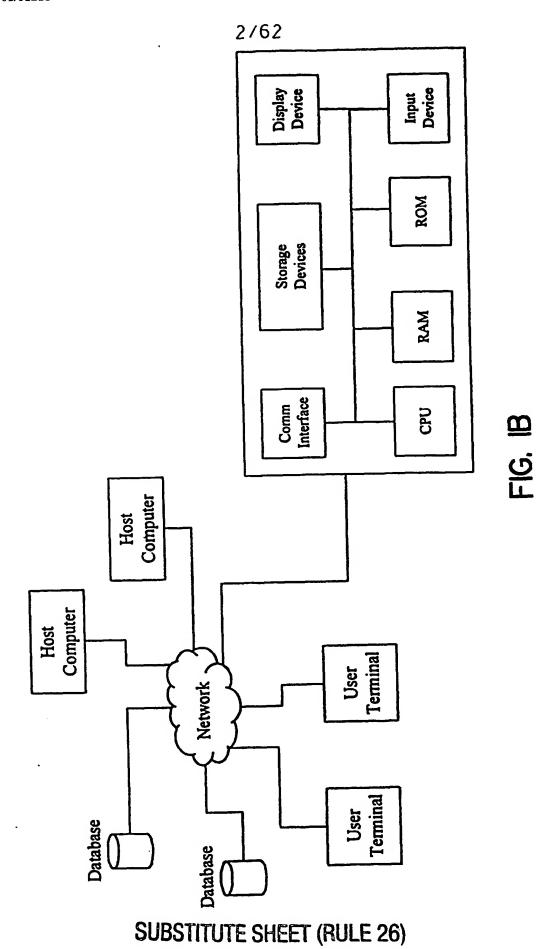
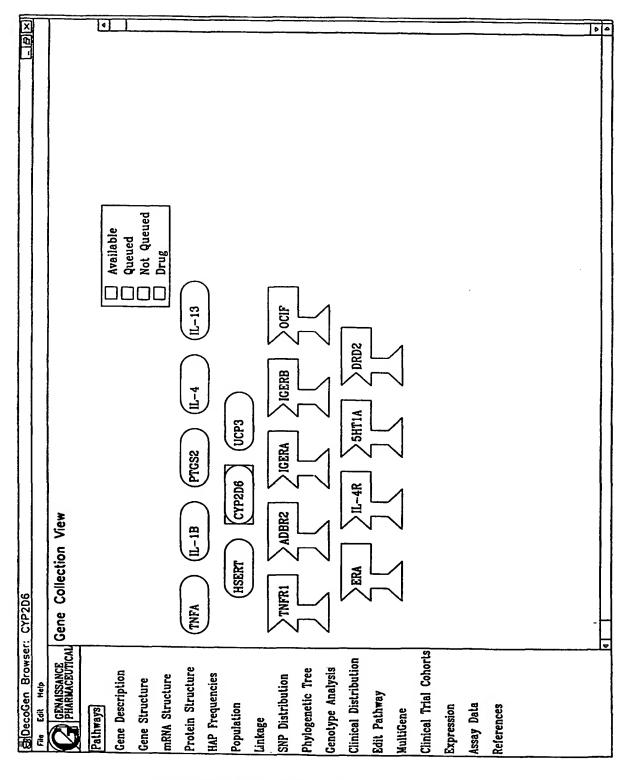


FIG. IA



3/62 **(3**)



**SUBSTITUTE SHEET (RULE 26)** 

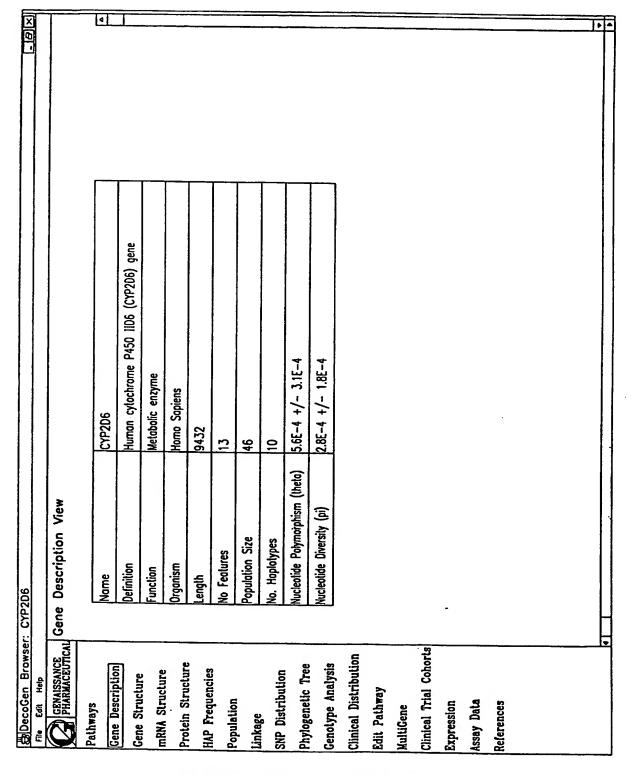
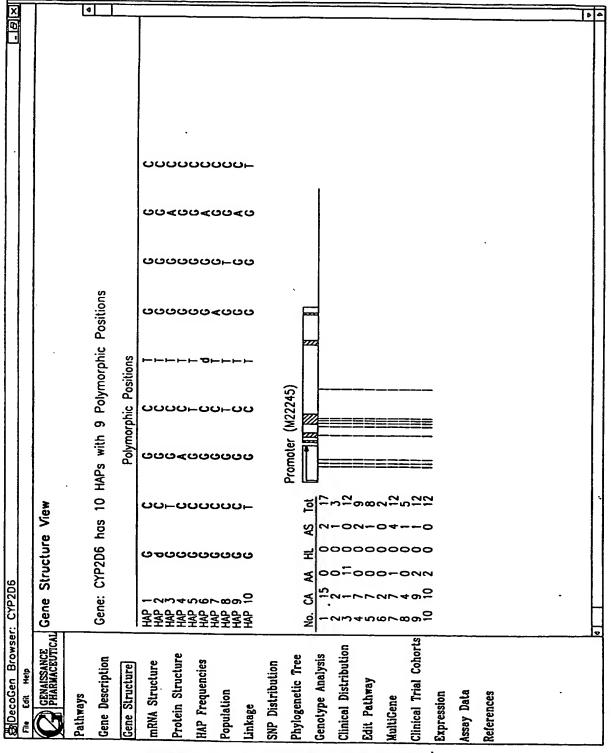
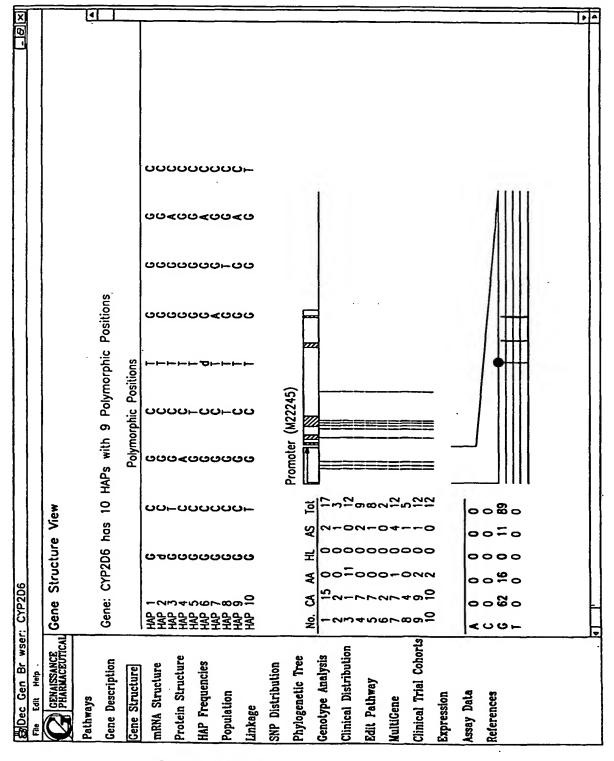


FIG. 4<sub>0</sub> 2<sub>0</sub>5



SUBSTITUTE SHEET (RULE 26)

FIG. 4b (2)/9

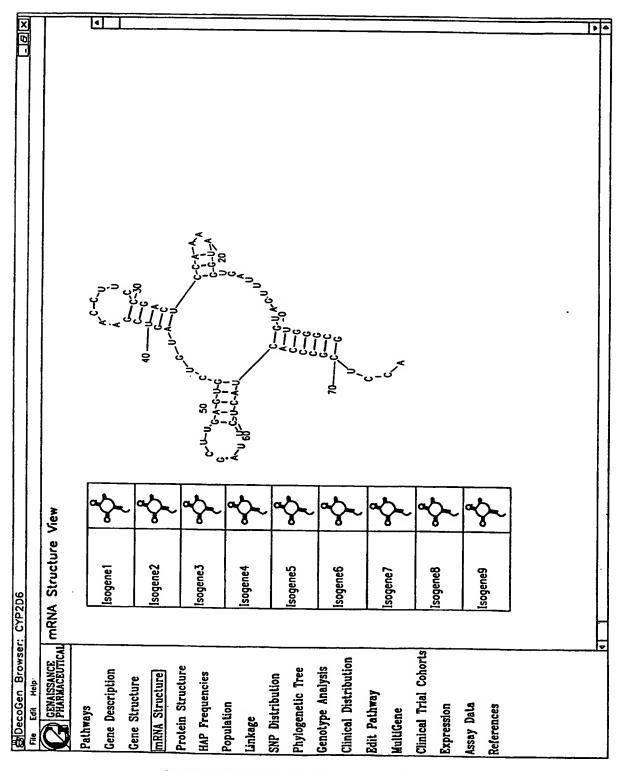


SUBSTITUTE SHEET (RULE 26)

	-	_	4 : 1 10101	_
		009		Redrow time= 10 ms
		290	acagacacacacacacacacatatectgaacacaggatectecatacgtteccaccagattetaateagaacatggaggeeggaan  begaacacacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacatggaggeeffgaao  begaacacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacatggaggeeffgaao  begaacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacatggaggeefgaao  begaacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacatggaggeefgaao  begaacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacactggaggeefgaao  begaacacacacacatatectgaacacaggatectecatacgtteccaccagattetaatcagaacactggaggeefgaao  begaacacacacacacacacacacaggatectecatacacgtteccaccagattetaatcagaacactggaggeefgaao  begaacacacacacacacacacacacaggatectecatacacgtteccaccagattetaatcagaacactggaggeefgaao  begaacacacacacacacacacacacacacacaggatectecatacacgtteccaccagattetaatcagaacactggaggeefgaao  begaacacacacacacacacacacacacacacacacacaca	Redro
		580	office of control of the control of	
		570		
		260	ctccotoacg ctccatoacg ctccatoacg ctccatoacg ctccatoacg ctccatoacg ctccatoacg	
		550	10000099900 10000099000 10000099000 10000099000 10000099000	
3388)		540	catatectga catatectga catatectga catatectga catatectga catatectga catatectga catatectga	
Cene (M3.	4	530	natocogcoc otocogcoc natocogcoc natocogcoc natocogcoc otocogcoc natocogcoc	
Alignment:	olour Catculate Help	520		
Gene Feature Sequence Alignment: Gene (M33388)	View Colour	510	######################################	
Feature	Font		12000000   P	
Gene	Edit		-26438786	ě
100	Ē		HAHAHAHAH ABABABABABABABABABABABABABABAB	done

FIG. 5

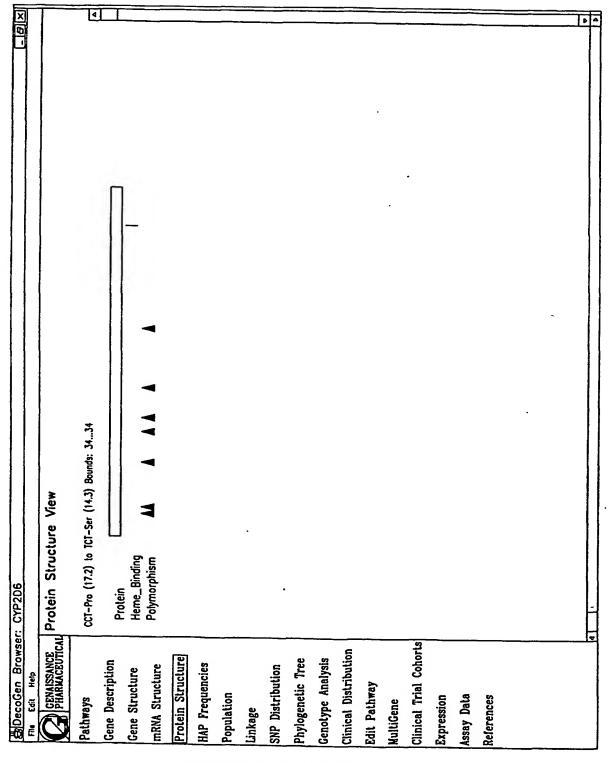
9



SUBSTITUTE SHEET (RULE 26)

9/62

~



10/62

 $\boldsymbol{\omega}$ 

<u>က်</u>

Blocogen Browser: CYP206	:YP206							- (B)X
File Edit Help.								
GENAISSANCE PO	Population View	A.						
Pathways	PID	Ethnicity	Age	Gender	HAP 1	HAP 2	Test	1
Gene Description	UP070	క	66	Ŀ	GCCTGGGC	GCCTGGC	0.1	
Gene Structure	UP072	ర	66	U.	dccctcccc	GCACTGGGC	0.2	
mRNA Structure	UP074	CA	66	<u>.</u>	GCGCTGGGC	GCACTGGGC	0.2	
Protein Structure	UP132	CA	66	¥	crecreer	GTGCTGGGT	0.3	
HAP Frequencies	UP133	క	66	М	GCCTGGC	GTGCTGGGT	0.2	
Population	UP134	<del>ر</del> ه	66	Ŀ	GCGCTGGGC	GCCTGGCC	0.1	
Linkage	UP137	క	99	<b>≥</b>	GTGCTGGGT	GTGCTGGGT	0.1	
SNP Distribution	UP009	క	66	L.	GCACTGGGC	GCACTGGGC	0.1	
Phylogenetic Tree	UP014	క	66	<u>t</u> e.	deecteece	GCGCTGGAC	0.3	
Genotype Analysis	UP020	క	99	Ŀ	GTGCTGGGT	GTGCTGGGT	0.2	
Clinical Distribution	UP021	క	66	×	ссеттетес	GCGCTGGGC	0.4	
Edit Pathway	UP022	క	66	≥	GCGCTGGAC	GCGCTGGAC	0.3	
MultiGene	OR001	ĄŞ	66	≥	deserteses	ccirrercc	0.2	
Clinical Trial Cohorts	OR002	<b>AS</b>	66	> 3	СССТСССС	GCGCTGGGC	0.3	
Expression	0R004	AS	66	<u>u</u>	GCACTGGGC	CCACTGGGC	0.2	
Assay Data	0R006	<b>AS</b>	66	Ŀ	ССЕТТСССС	GCGCTGGAC	0.1	
References	WT003	ర	66	LL.	ссетсес	ссеттетес	0.2	•
٠	WT005	ర	66	<b>-</b>	ссеттевес	GCGCTGGGC	0.2	
	WT007	ర	66		сстетес	ссеттелес	0.4	
	UP012	ర	66	L.	GCGCTAGGC	GCGCTGGAC	0.1	
	UP135	ర	66	Σ	GCACTGGGC	GCGCTGGAC	0.2	Ī
								1

531 Rec'd PCT 2 6 DEC 2001

## This page is not part of the pamphlet!

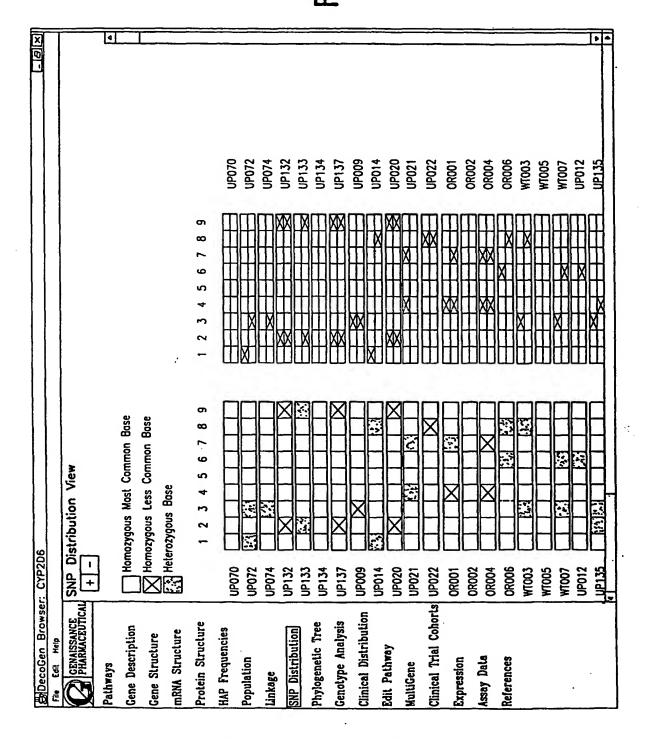
WO 01-01218 3/3

Date: 04 jan 2001

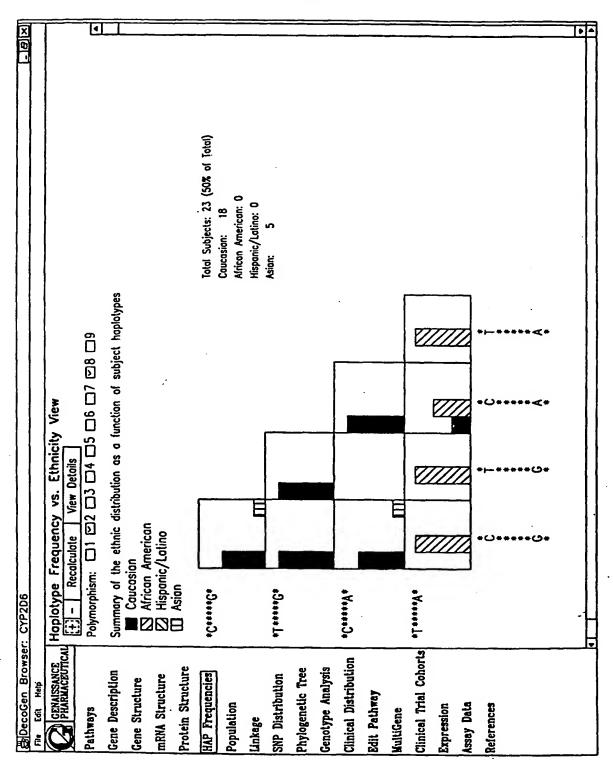
**Destination: Agent** 

11 / 62

F1G. 9

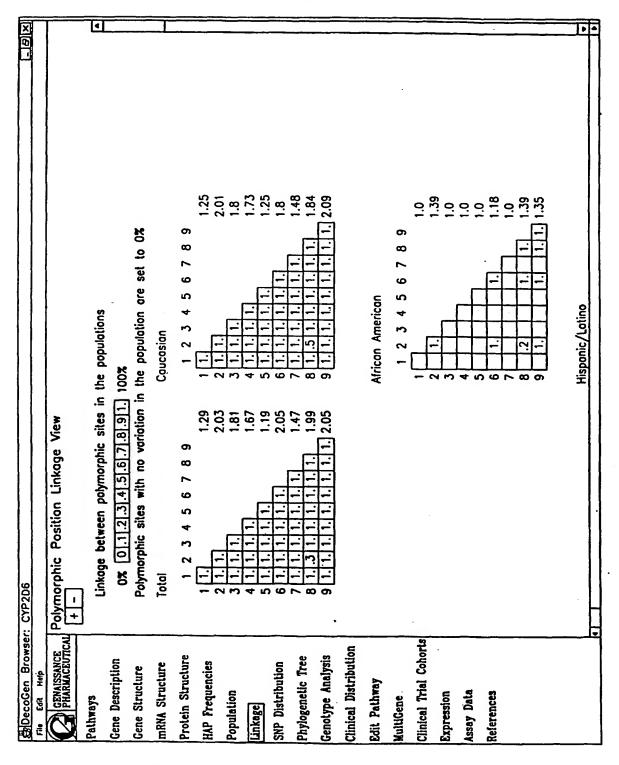


12 / 62 **Q 9** 

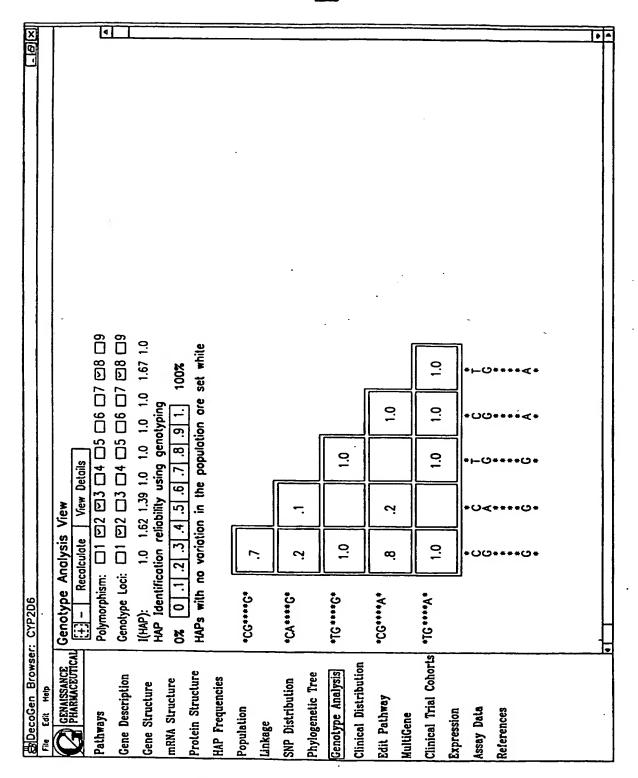


<u>5</u>

: CYP2D6			2						X 9 -
GENAISSANCE   Hoplotype Frequency vs. Ethnic   PHARMACEUTICAL	icy vs.   Wew Si	Ethnicity mmany   12 C	Ethnicity View (mmon)	8 	_				[4]
Details of the ethnic distribution as a function of subject haplotypes	thnic distribution as a	Ę	tion of subjec	ct hopi	otypes				
3 Columns are given for each Ethnogeographic group: Total number sampled with HAP pair	ore given for each Eth Imber sampled with HAF	5. g	geographic gra air	:dnc					
Fraction of the ethnogeographic group with that HAP pair Fraction expected under Hardy-Weinbera equilibrium for that HAP	of the ethnogeographic expected under Hardv-		roup with that inberg equilibr	HAP I	poir or that HAP pair				
HAP 1 HAP 2	HAP 2		'z	XPop.	Coucosion	African American	Hispanic/Latino	/Lotino	\$
*********************************	*D*****O*			20%	18 56.3% 37.9%	0.0%	0.0%	0.0%	2
**************************************	*O****O*		2 4%		6.3%	0 0.0% 2.4%	0 0.0%		0
	. 9				%C.71	0.0%			5
			o +		12.5%	0.0%			_ (
**************************************	* C * * * * C *		0.4		3 9.4% 4.2%	0 0.0% 2.4%	0.0	0.0%	
-	*5***** L*				200	25.0%			-
_	*V******		3 6%		1 3.1% 1.1%	25.0%	000	0.0%	0
* V***** L* * V***** L*	* V***** L*		3 6%		0 0.0% 0.1%	3 37.5% 37.9%	0 0.0%	0.0%	-
					-				
					`				
									_
-									
									J.
									Ē



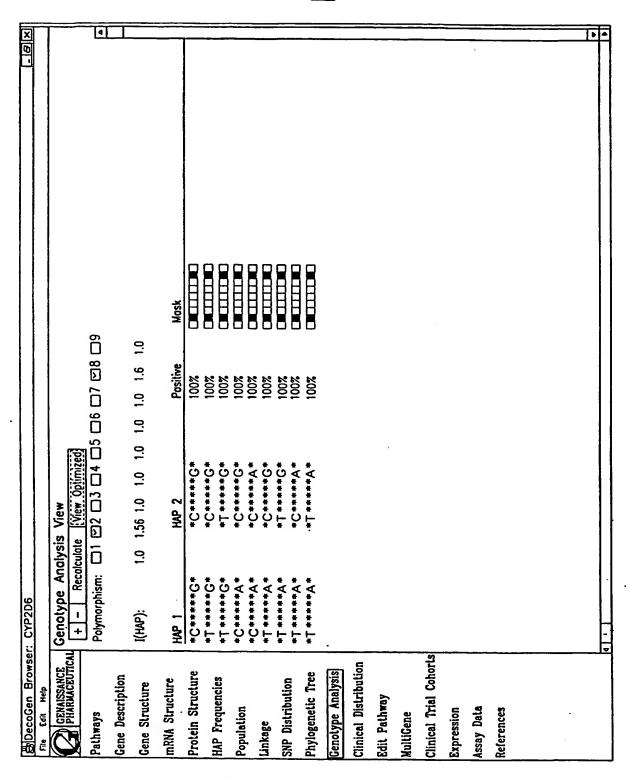
SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

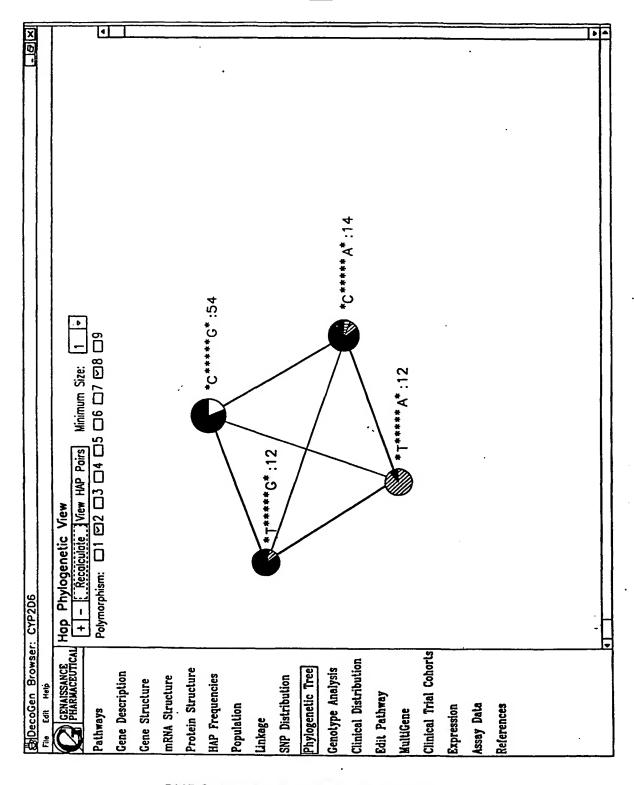
Sploec Gen Br wser: CYP2D6	: CYP2D6				X(6) =
File Edit Help					
GENAISSANCE PHARMACEUTICAL	Genotype Analysis View	s View Optimized			
Pathways	Polymorphism: 1	©2 □3 □4 □5 □6	□7 ⊡8 □9	•	4
Gene Description	Genotype Loci:	©2 □3 □4 □5 □6	口7 四8 口9	•	
Gene Structure	I(HAP): 1.0	1.56 1.0 1.0 1.0 1.0	1.0 1.6 1.0		
	HAP 1	HAP 2	N XPop.	p. Positive	
Protein Structure	*9*****0*	*5*****5*	_		
HAP Frequencies	******	**************************************	2 4 2 4 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2	100%	-
Population	*C*****A*	*9*****3*		100%	
	*C*******	* <b>V</b> * * * * * * * * * * * * * * * * * * *		100%	
	* V * * * * L *	**************************************	v7 C	*00¢	
	*V***** L*	*V******		2007	
Phylogenetic Tree	* Y***** L*	* V***** L*	3 6%	100%	
Genotype Analysis					
Clinical Distribution	·				-
Edit Pathway					
MultiGene					
Clinical Trial Cohorts					
Expression					
Assay Data					
References					
			•		
- 15					

17 / 62 <u>ග</u>



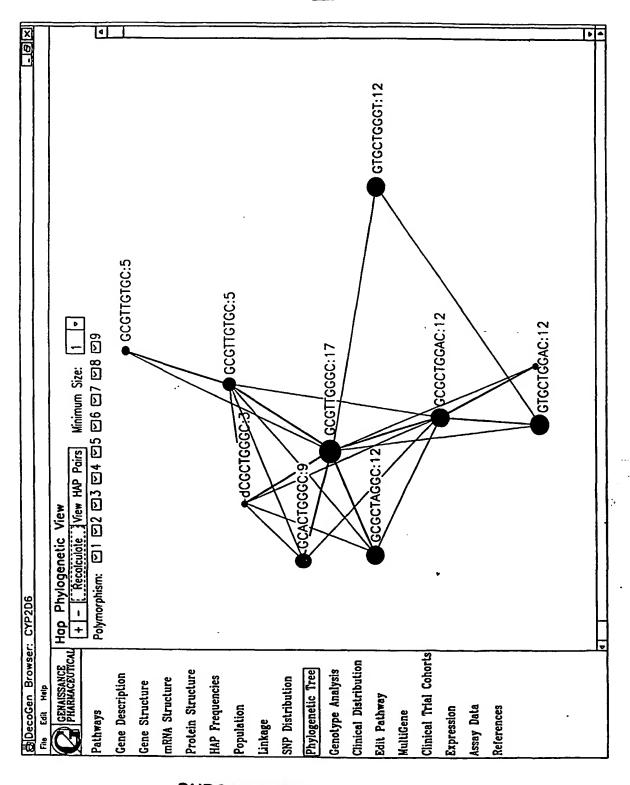
WO 01/01218

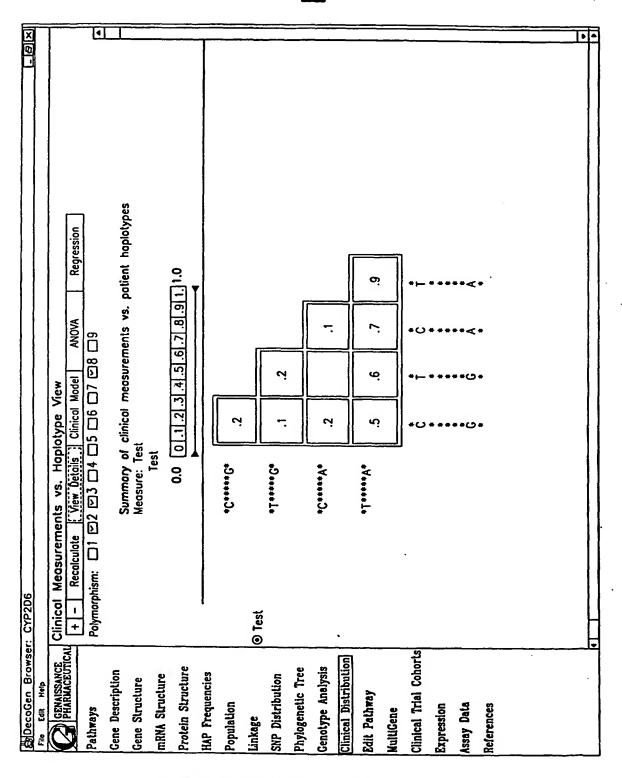
PCT/US00/17540



SUBSTITUTE SHEET (RULE 26)

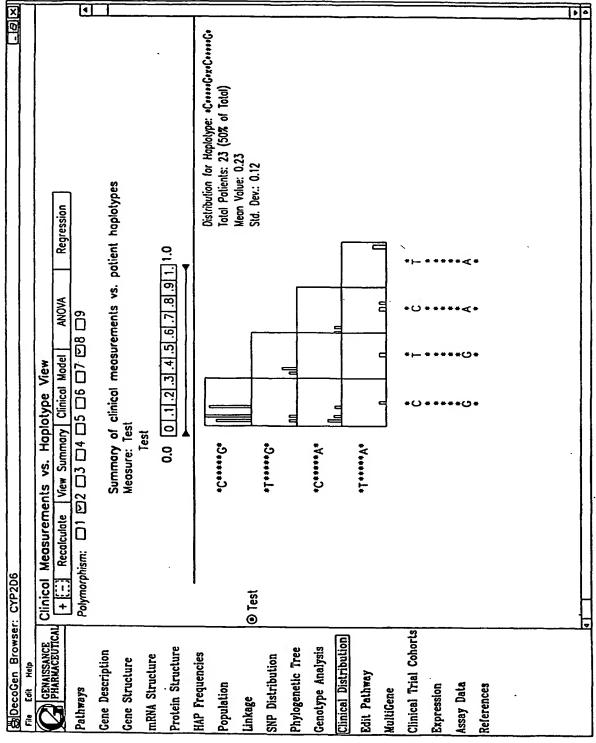
19 / 62 **'2** 





SUBSTITUTE SHEET (RULE 26)

21/62 FIG. 19



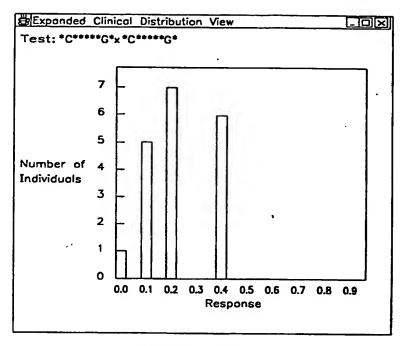


FIG. 20

inical	Measure	ments Re	gression (	Calculation		
Site	Slope	Intercept	Vorionce	T(slope)	Significance Level	
1	-0.083	0.316	0.05	-0.59	0.7223	
2	0.154	0.231	0.04	4.22	0.9999	
3	-0.08	0.326	0.05	-1.16	0.8735	
4	-0.0080	0.313	0.06	-0.14	0.5572	
5	0.145	0.305	0.05	0.86	0.804	
6	-0.08	0.332	0.05	-1.24	0.8902°	
7	0.0070	0.31	0.06	80.0	0.5303	
8	0.158	0.222	0.04	4.34	1.0	
9	-0.043	0.322	0.05	-0.76	0.7752	

FIG. 21

Dec Gen Browser: CYP2D6	r: CYP2D6										XØ:
File Edit Help											
GENAISSANCE PHARMACEUTICAL	Clinical + -	Meas	ents vs. Haplotype View View Distribution Clinical Model	View I Model ANOVA	Regr	Regression					
Pathways	Polymorphism:			□7 ⊡8 □9							1
Gene Description		Sur	nmory of clinica	Summary of clinical measurements vs. patient haplotypes	patient h	aplotype	တ္				
Gene Structure		Mec	Meosure: Test Test								
mRNA Structure			ا		ĺ						_
Protein Structure			0.0	.3  .4  .5  .6  .7  .8  .9  1.	<u>.</u>						
HAP Frequencies	ł		`		,						T
Population	© Test	\$		Hop 2	2	¥Pop.	Mean	Stddev X 2	X2	0(x=2 K-3)	a -
Linkage		٠ *	*5*****	*9*****0*	23	20%	0.24	0.12	9.17	_	
CWD Distriction		•	*D*****L*	********	7	4%	0.15	0.07	0.0	_	
מער עוצנרוטענוסח		L*	*5*****	*******	4	8%	0.5	0.08	0.0	1.0 (-3)	
Phylogenetic Tree		<u>.</u>	*C*****	*5*****	വ	10%	0.22	0.13	O.8	_	
Cenotone Analysis		<b>O</b> (	*C****A*	CA.	ю. '	22	0.13	0.15	0.0	_	
delictype Allarysis		<u>-</u> 1	. V		<b>-</b> (	2%	0.5	0.0	0.0	_	
Clinical Distribution			* \	*1****C*	7 -	4% %	0.55	0.0	0 0	_	
Edit Pathway		i de	· V	****** ******	ט ניו	% 9%	0.93	0.0	0.0	5 0 5 0 5 0 5 0 5 0 5 0 5 0 5 0 5 0 5 0	
MultiGene											
Clinical Trial Cohorts											
Expression											
Assay Data	⊙ Test			•							
References											_
											Ŧ
											1

	osurements .				
olymorphism	: 🗆1 🖾2 🗆	3 🗆 4 🗅	⊃5 □6 Œ	27 図8 🗆 9	
Source of Va			es F-ratio		
Between Grou	ips 7	0.26	19.65		
Within Groups	37	0.01	13.03		
Critical F-Dis	tribution Value 902	£ 1.88			- 1
0110001 7 012	tribution Value 95%				
J. 1. J.	tribution Value 997				
Critical 1-Dis					
Significant be	etween-group varia				
Significant be	etween-group varia etween-group varia	tion at the	95% confide	nce level	
Significant be	etween-group varia	tion at the	95% confide	nce level	
Significant be	etween-group varia etween-group varia	tion at the	95% confide	nce level	
Significant be Significant be Significant be	elween-group varia elween-group varia	tion at the tion at the	95% confide 99% confide	nce level	_
Significant be Significant be Significant be	etween-group vana etween-group vana etween-group varia HAP 2	tion at the tion at the N	95% confide 99% confide Average	nce level nce level Std. Dev.	_
Significant be Significant be Significant be	etween-group varia etween-group varia HAP 2 *C*****G*	tion at the tion at the N 23	95% confide 99% confide Average 0.23	nce level nce level Std. Dev. 0.12	_
Significant be Significant be Significant be HAP 1 *C*****G*	etween-group variatiween-group variati	tion at the tion at the N 23 2	95% confide 99% confide Average 0.23 0.15	std. Dev. 0.12 0.07	-
Significant be Significant be Significant be HAP 1 *C*****G* *C*****G*	etween-group variativeen-group	tion at the tion at the N 23 2	95% confide 99% confide Average 0.23 0.15 0.22	Std. Dev.  0.12 0.07 0.13	_
Significant be Significant be Significant be Significant be Cesses Ge Cesses Ge Cesses Ge Tesses Ge Tesses Ge	etween-group variateween-group	tion at the tion at the N 23 2 5 4	95% confide 99% confide Average 0.23 0.15 0.22 0.2	Std. Dev.  0.12 0.07 0.13 0.08	_
Significant be Significant be Significant be HAP 1  *C**********************************	etween-group variatelween-group	tion at the lion at the N 23 2 5 4 2	95% confide 99% confide Average 0.23 0.15 0.22 0.2 0.55	Std. Dev.  0.12 0.07 0.13 0.08 0.07	

FIG. 23

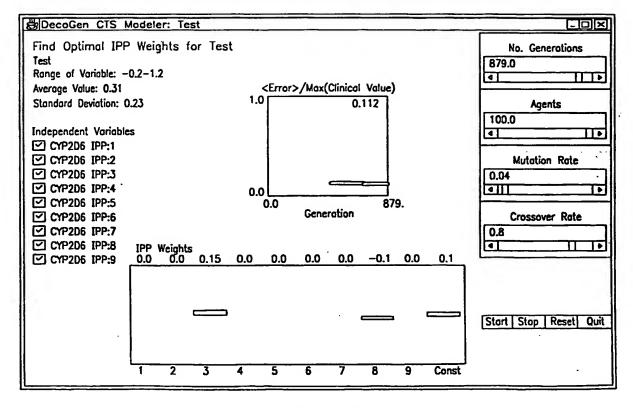
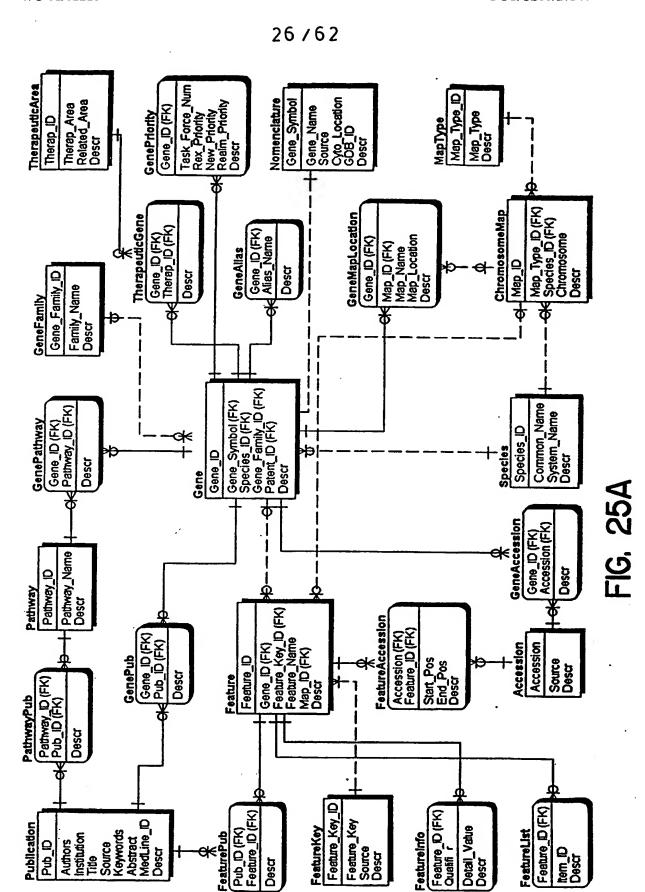
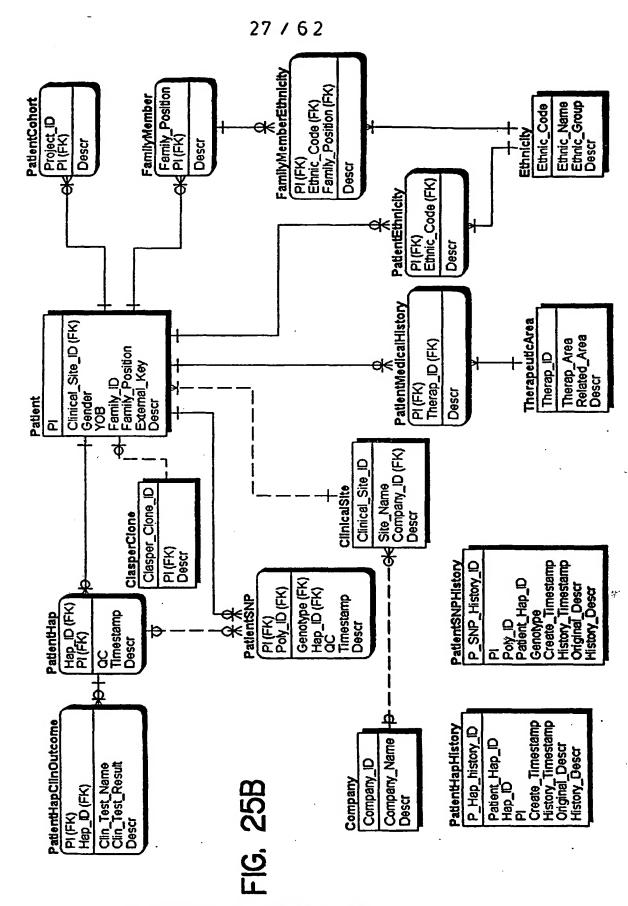


FIG. 24
SUBSTITUTE SHEET (RULE 26)

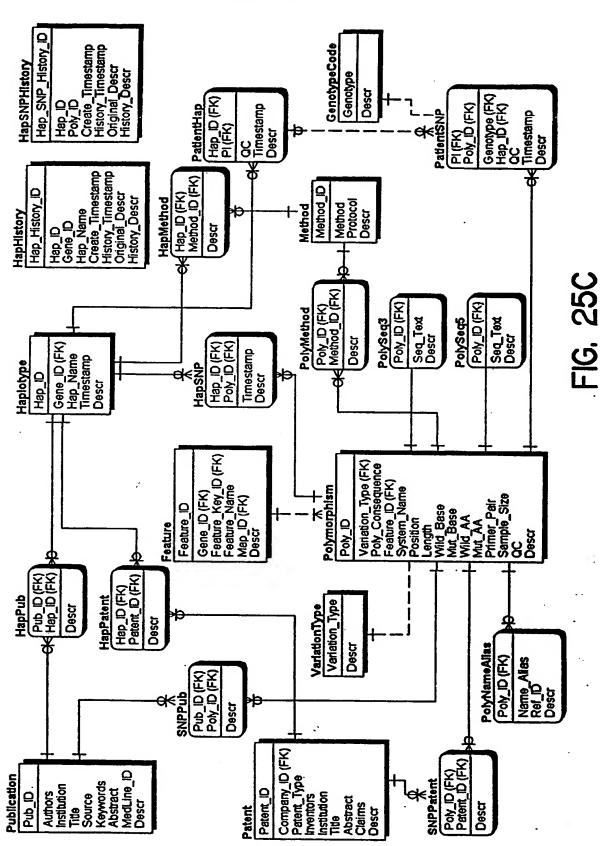


SUBSTITUTE SHEET (RULE 26)



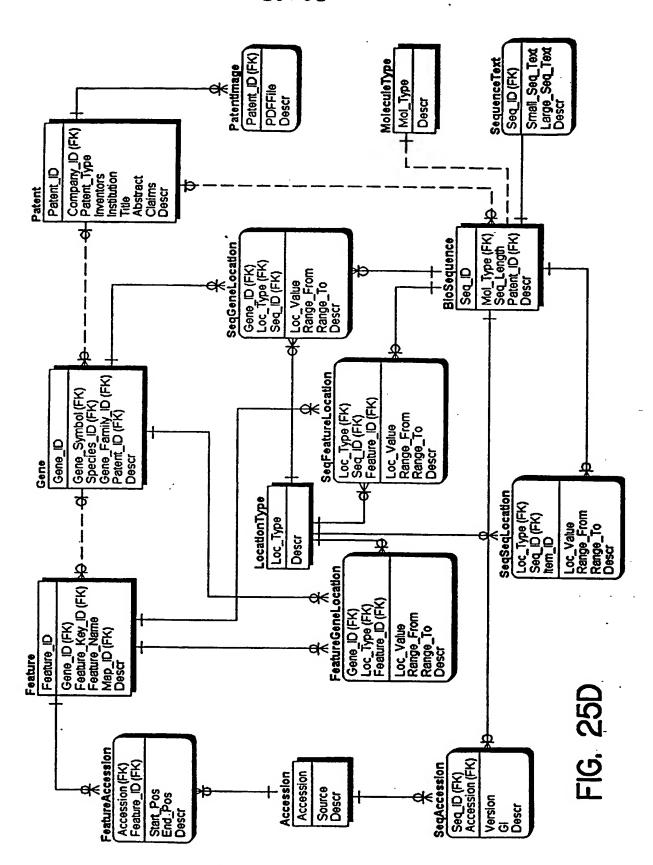
SUBSTITUTE SHEET (RULE 26)

28 / 62

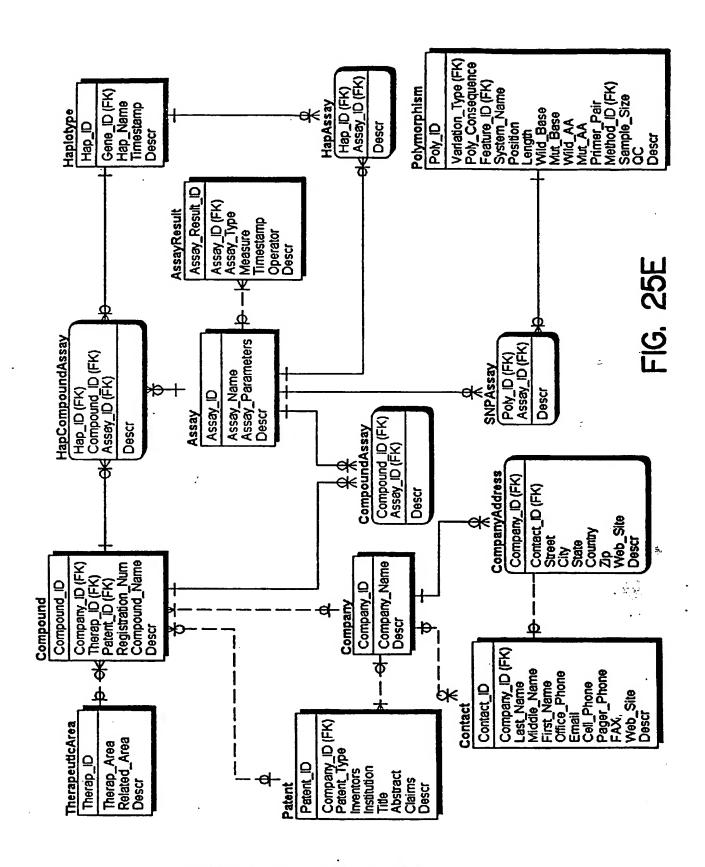


SUBSTITUTE SHEET (RULE 26)

29/62



SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

## Legend of Figures:



Rectangle Boxes: Tables in the database.



Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

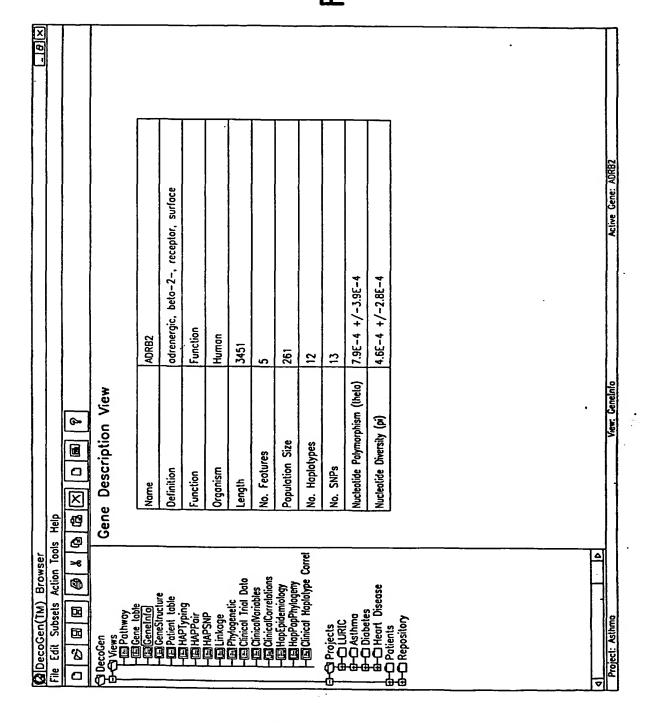
- 2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: >-- On-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: K Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 8: ----- Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.
- Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: ----- Non-identifying parent / child relationship. It represents the nullable o-or-1-to-exact-1 relationship.
- 14: \(\frac{1}{2} \frac{1}{2} \)
  Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

## FIG. 25F

32/62

(C) DecoCen(TM) Browser				× θ -
File Edit Subsets Action Tools Help	ıls Help			
		& <b>(a)</b>		
Coccocen Coc	Pathway View: Asthma	Asthma Extracellular OADBR2		
CinicalCorrelations  El HapEpidemiology		Intracellular		
The nuproperty Correl  The Clinical Haplotype Correl			OPDEGB	OIL9
## Control of the con			OCALM1	OJAK3
4		Vew., Politwoy	Active Gene: ADRB2	РЯВ2

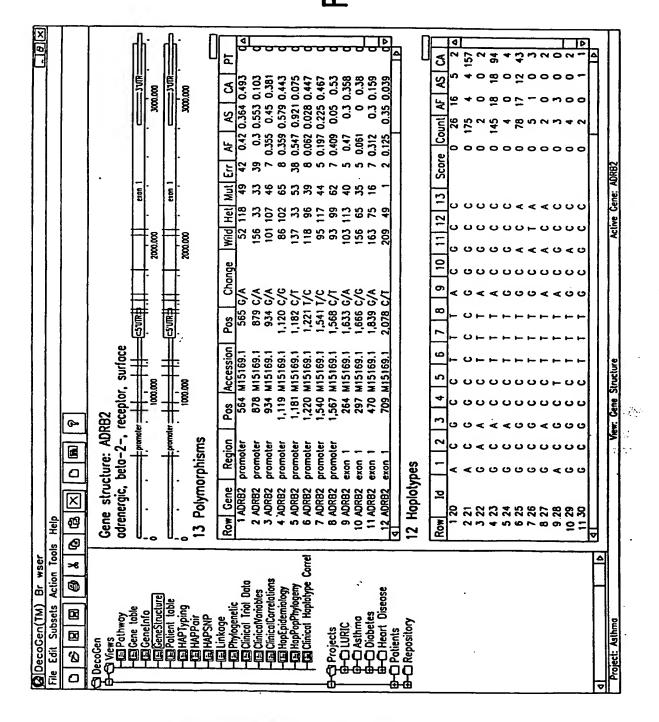
SUBSTITUTE SHEET (RULE 26)



**SUBSTITUTE SHEET (RULE 26)** 

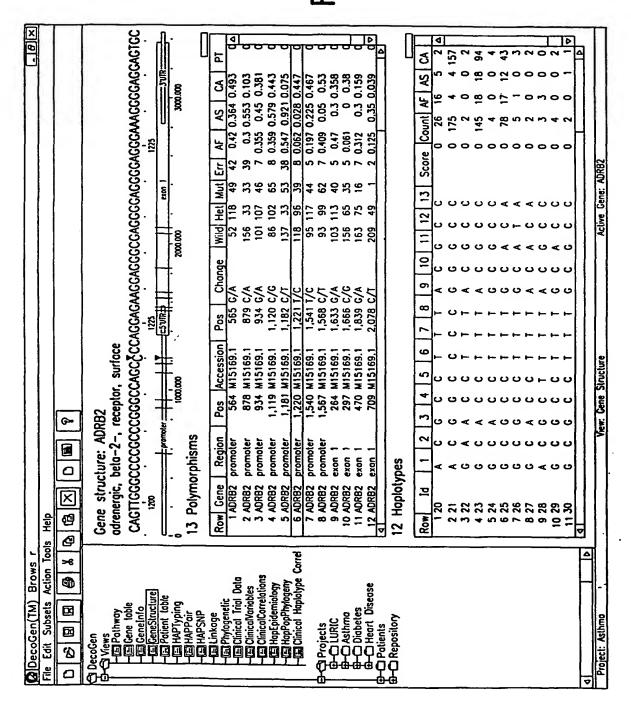
34 / 62

FIG. 28A



**SUBSTITUTE SHEET (RULE 26)** 

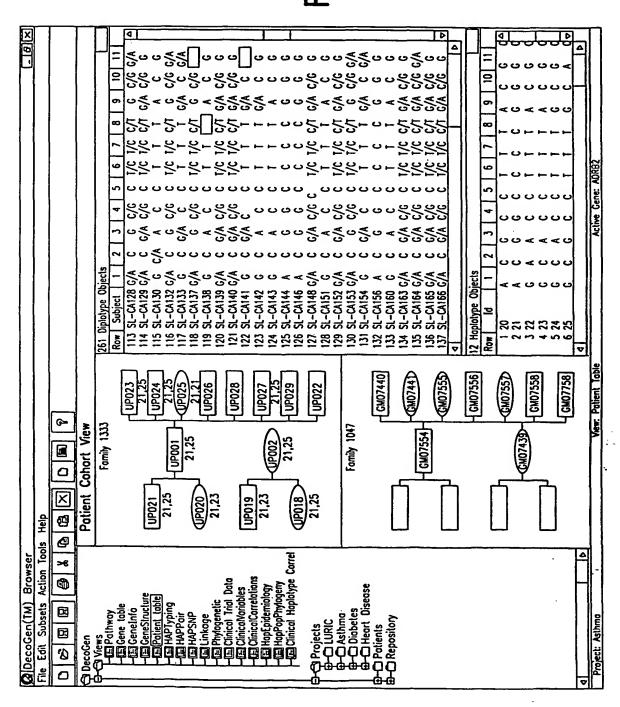
FIG. 28B



SUBSTITUTE SHEET (RULE 26)

36 / 62

FIG. 29A



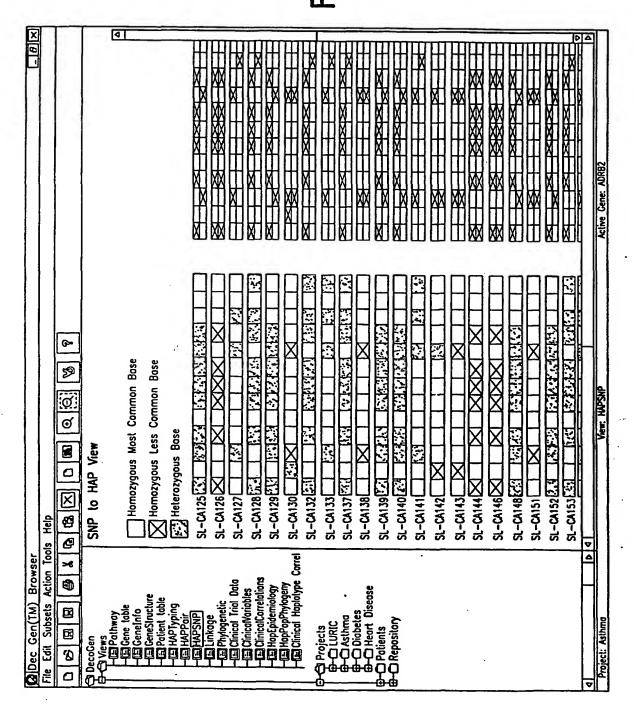
SUBSTITUTE SHEET (RULE 26)

FIG. 29E

MajDecoGen(IM) Browser												ΘİX
File Edit Subsets Action Tools		Help										
	8	<b>B</b> 区	G									
G DecoGen		Clinical Trial Data	Oato									
- Coviews	182	82 PotientMeasurement Objects	ent Objects									L
Tel Cone toble	Row	w Potient	Severity Skin	Skin Tes	FVC LP	FVC %P	FEV1 L.	FEV1 7	FEV1/FV	FEF PRE	FEF %P	
- El Geneinfo	_	1SL-AA131	2.0	1.0	1.88	58.0	1.28	52.0	0.89	0.83	49.0	1.8
- (E) GeneStructure		2 SL-AA134	2.0	1.0	2.01	54.0	0.96	34.0	48.0	0.45	12.0	2.2
Patient toble	L	3 SL-AA136	0.0	0.0	2.56	89.0	2.22	93.0	87.0	3.2	91.0	2.5
HE HAPTyping		4 SL-AA150	2.0	1.0	1.4	50.0	9.0	27.0	43.0	0.22	7.0	5:
Tell HAPPoir	_	5 SL-AA155	2.0	0.1	1.77	40.0	0.98	27.0	55.0	0.61	16.0	2.2
HE HAPSNP	_	6 St-AA159	2.0	0:1	2.89	999	1.7.1	51.0	59.0	6.0	20.0	4.
-E Linkage	L		1.0	0.1	4.28	96.0	2.7	79.0	63.0	1.48	33.0	5.2
Phylogenetic		8 SL-A4211	1.0	1.0	3.44	91.0	1.97	0.99	57.0	1.39	32.0	5.5
EClinical Irial Data	_	9 SL-AA227	2.0	0.0	1.93	54.0	96.0	37.0	49.0	0.35	11.0	2.5
-(E) Clinical Variables	<u></u>	10 SL-AA253	1.0	0.	3.0	0.96	2.0)	70.0	57.0	0.99	25.0	3.8
TIE Clinical Correlations		1 SL-AA270	dИ	dΝ		d N	dΝ	₽	dί	g≥ Z	g. ₽	<u>₽</u>
The Hopepidemiology		12 SL-A4275	ďΝ	d <sub>N</sub>		d N	<u>S</u>	₽	ď	d S	<u>Q</u>	<u>S</u>
Cipical Maplabae Correl		13 SL-CA101	1.0	1.0	2.17	85.0	1.92	64.0	71.0	1.33	38.0	3.2
and adjoint in the second		14 St-CA103	2.0	1.0	3.56	59.0	2.16	46.0	61.0	1.13	18.0	<del>1</del> .
De Ca Projects		15 SL-CA104	2.0	0.0	2.76	57.0	1.46	39.0	53.0	0.59	16.0	3.4
D-O LURIC		16 SL-CA105	2.0	0.0	1.99	62.0	1.11	46.0	57.0	0.55	24.0	2.3
the DAsthmo	-	17 SL-CA106	0.0	1.0	3.46	82.0	5.69	83.0	57.0	2.28	51.0	4.4
Operates Dispetes		18 SL-CA107	0.0	0.1	3.82	113.0	2.59	83.0	78.0	1.7	46.0	3.9
H⊕ Heart Disease		19 SL-CA108	ΝÞ	dN	dΝ	NΡ	NP	JND.	ΝP	NP	NP	₽
← Potients	7	20 SL-CA109	1.0	1.0	2.63	93.0	1.7	7.0	64.5	0.89	25.0	2.8
⊕ C Repository	_	21 SL-CA110	0.0	1.0	4.56	114.0	3.18	101.0	70.0	2.24	51.0	4.5
	7	22 SL-CA111	2.0	1.0	3.08	0.69	2.01	58.0	65.0	1.12	32.0	3.3
	7	23 SL-CA114	1.0	0:0	2.83	84.0	2.18	77.0	77.0	1.77	43.0	0.
	Ž	24 SL-CA116	1.0	0.	2.44	83.0	1.91	79.0	78.0	89.		₹]
	7	25 SL-CA117	0.1	0.1	3.81	90.0	2.25	67.0	59.0	1.04	22.0	÷.
	7	26 SL-CA118	1.0	1.0	1.53	76.0	1.27	71.0	83.0	1.27	49.0	9.
	7	27 SL-CA119	<u>₹</u>	g⊾	<b>₽</b>	٩	<u>S</u>	S S	<u>R</u>	g.	g.	9
	7	28 SL-CA120	0.0	1.0	4.24	106.0	17.7	83.0	64.0		33.0	4.4
	7	29 SL-CA121	1.0	0.0	3.05	88.0	1.9	70.0	62.0	0.95	26.0	3.6
	~	30 SL-CA122	0.0	1.0	5.76	105.0	4.35	103.0	75.5		62.0	6.0
		31 SL-CA123	2.0	1.0	1.82	0.99	0.92	40.0	50.0		12.0	2.5
	3	32 SL-CA124	2.0	0.0	2.45	29.0	1.3	43.0	53.0	0.41	11.0	2.5
	~	33 SL-CA125	2.0	1.0	1.19	42.0	0.81	37.0	68.0		22.0	ij
•	~	4 SL-CA126	2.0	0.0	1.74	64.0	11.17	52.0	67.0			1.8
4	_ ▽	15 S -CA127	d d	10	197	18.7	163	1730	830	1 49	999	3
Project: Asthmo	╕		View: Chr	Very: Clinical Inol Data	l ste			Active Gener ADRB2	ADRB2			
	ļ											

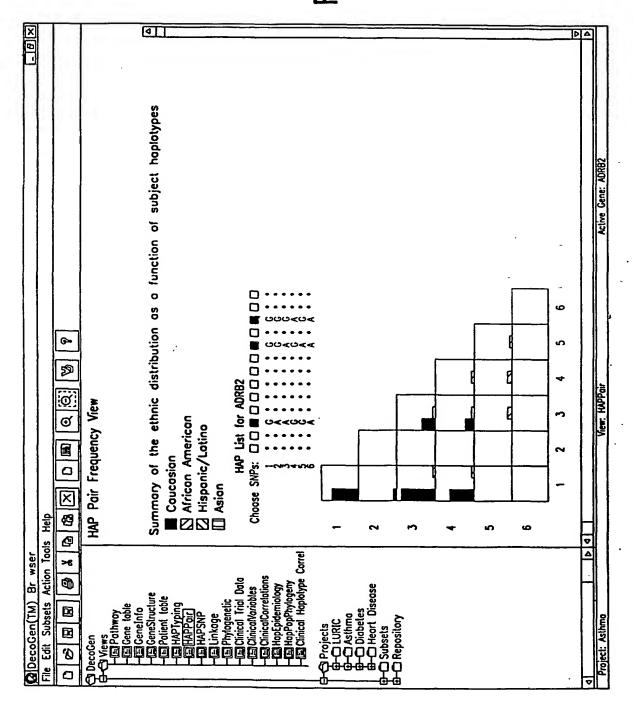
SUBSTITUTE SHEET (RULE 26)

FIG. 30



SUBSTITUTE SHEET (RULE 26)

-1G. 3



SUBSTITUTE SHEET (RULE 26)

FIG. 32

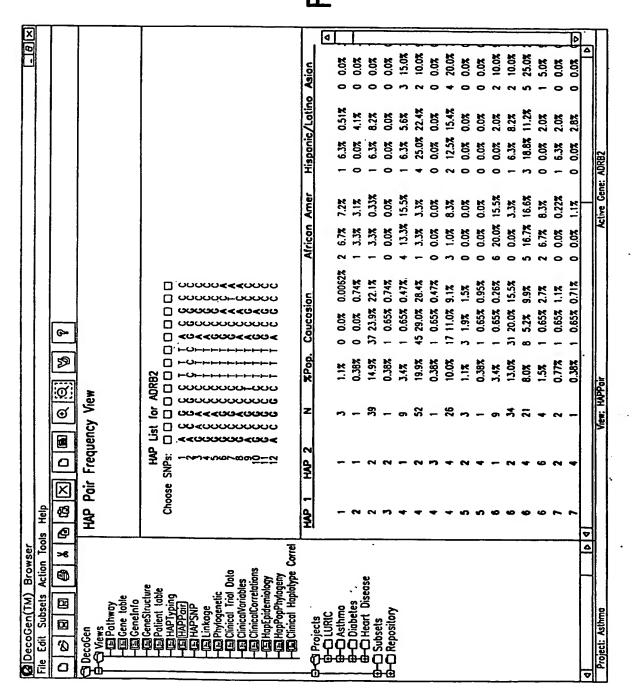
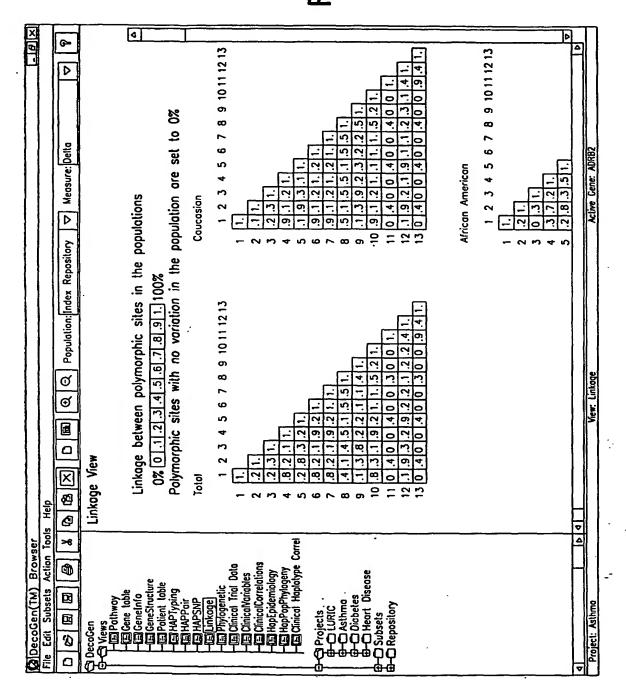


FIG. 3



SUBSTITUTE SHEET (RULE 26)

42/62

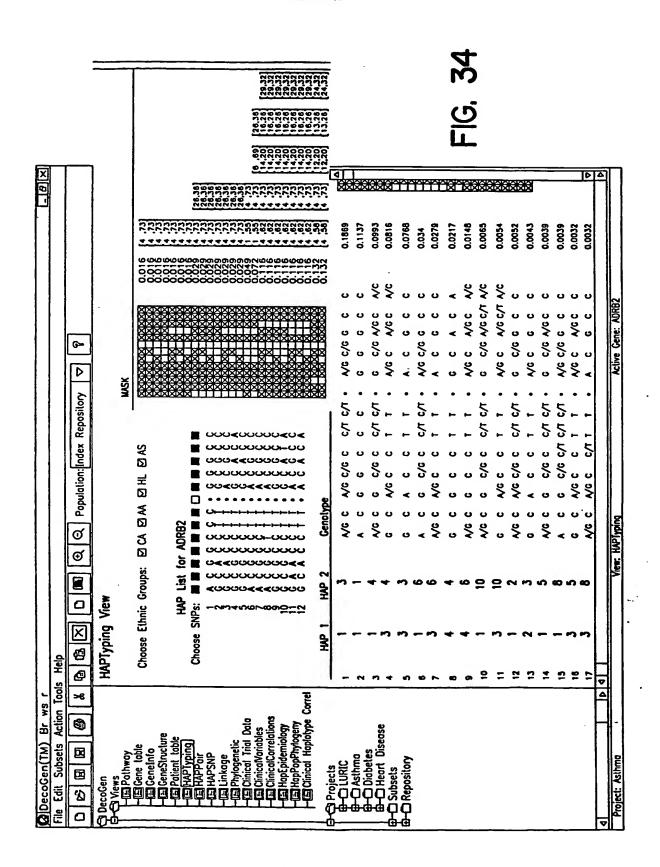
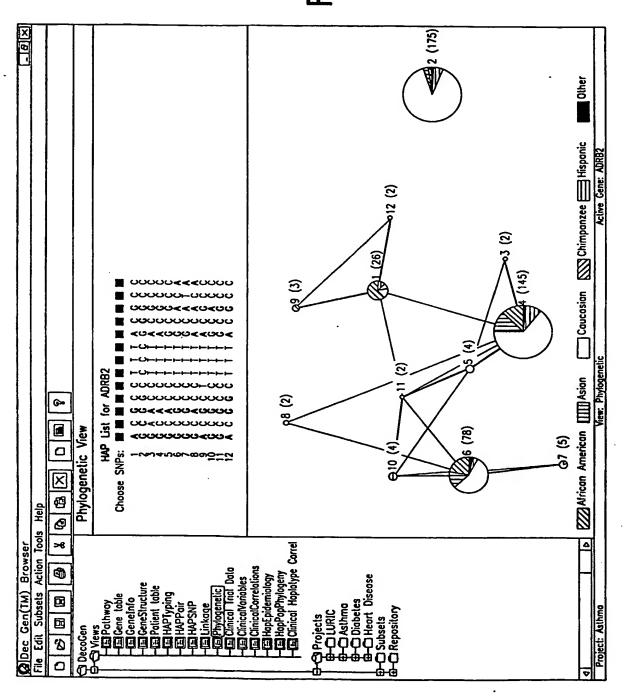


FIG. 35



SUBSTITUTE SHEET (RULE 26)

44/62

FIG. 36

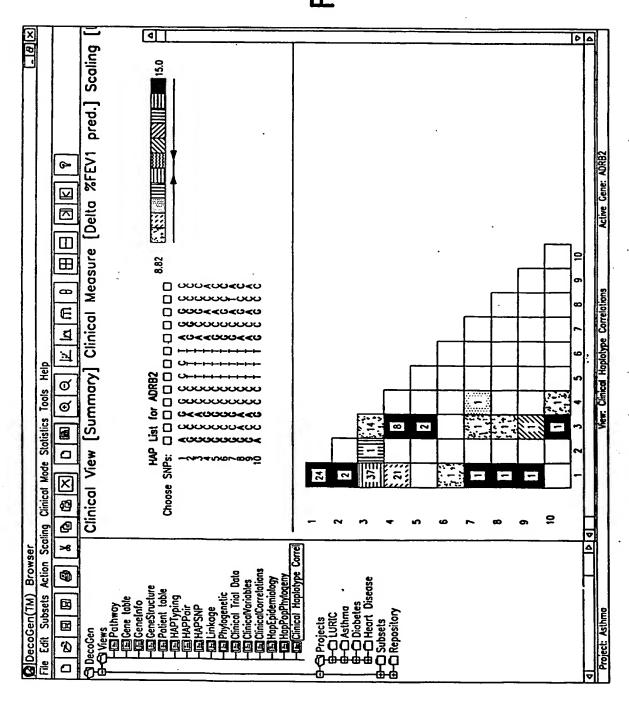
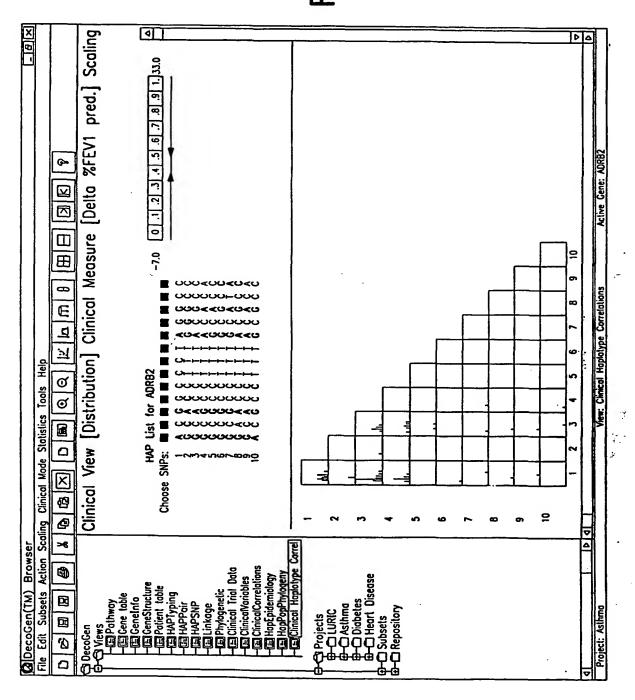


FIG. 37



SUBSTITUTE SHEET (RULE 26)

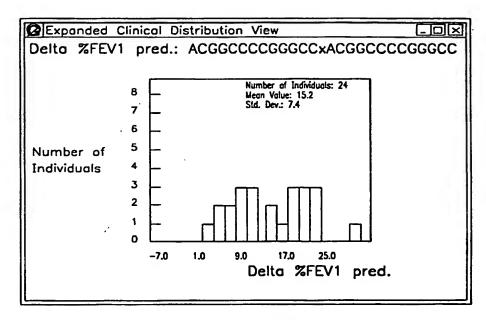


FIG. 38

DecoGen Single Ger	e Statistics	Calculato	r				[_]	
Show/Hide ]	CC Line							
Gene: odrenergic,	beta-2-, r	eceptor,		Clinic 0.05 0.1		ure: Delta % te: -4	FEV1 pr	d.
Regression Resu	ilts Intercept	Slope	Slope Ran	ge	R** 2	Corr. Coef (R)	P-value	
+G++++++G+++   ++++++A+G++   ++A+++++A+G++   ++A++++A+G++   ++A++++A+G++   ++A++++A+G++	10.501 10.526 14.583 14.471 14.626 14.615 14.6	1.99 1.956 -2.206 -2.048 -2.241 -2.308 -2.343	-0.08 -0.11 -4.28 -4.13 -4.32 -4.4 -4.46	4.06 4.02 -0.13 0.032 -0.16 -0.21 -0.22	0.0301 0.0293 0.0365 0.0315 0.0374 0.0391 0.0394	0.1734 0.1711 -0.1911 -0.1774 -0.1934 -0.1977 -0.1984	0.0297 0.0314 0.0187 0.0268 0.0175 0.0156 0.0153	
				*****				

FIG. 39A

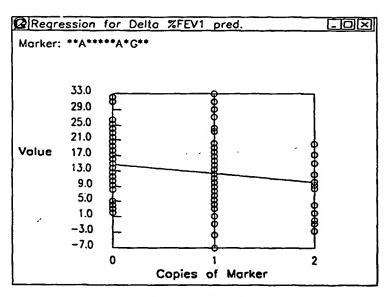
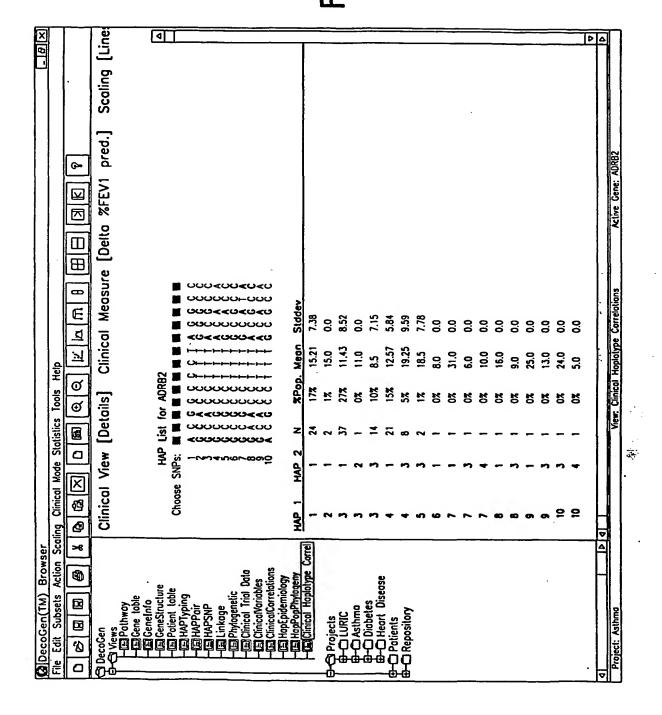


FIG. 39B

FIG. 40



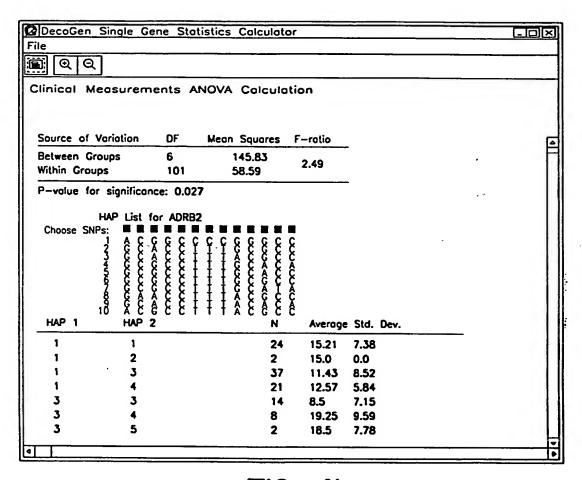
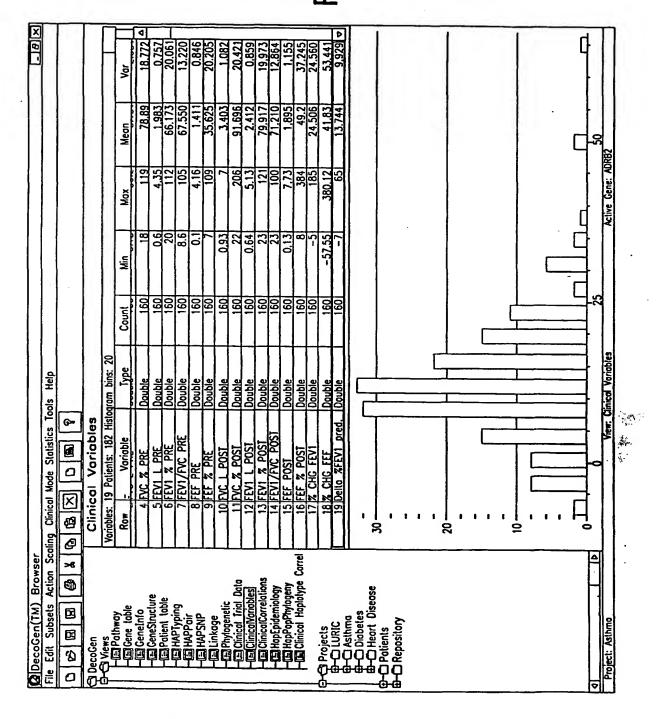


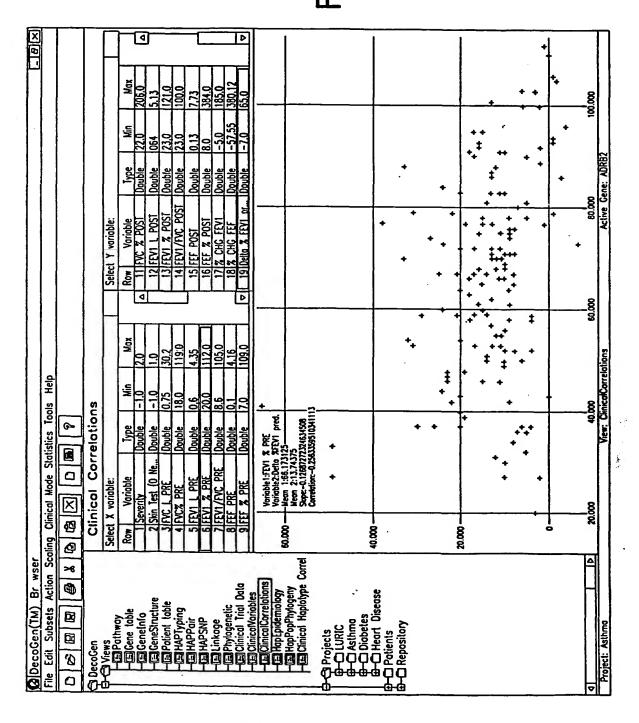
FIG. 41

FIG. 42

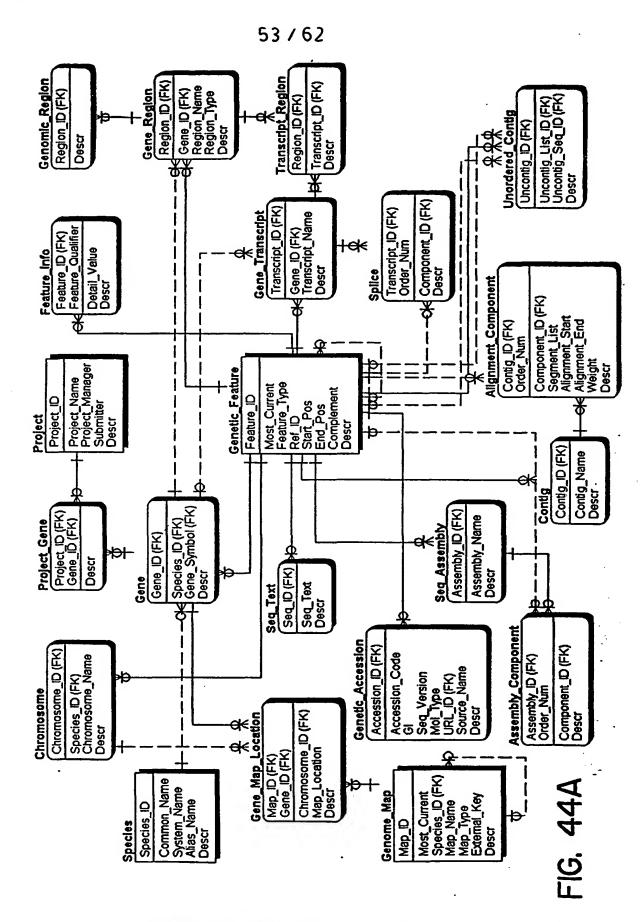


SUBSTITUTE SHEET (RULE 26)

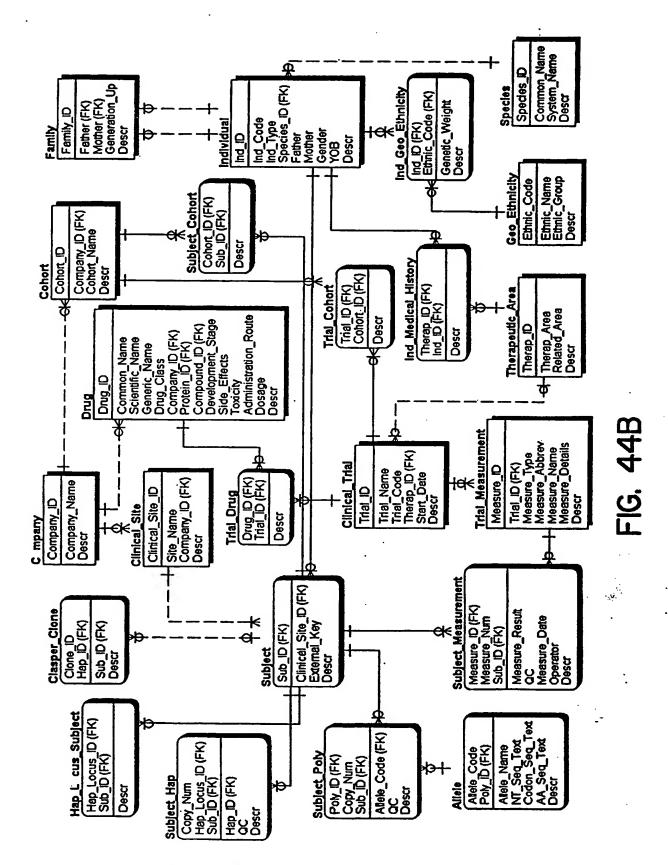
FIG. 45



SUBSTITUTE SHEET (RULE 26)

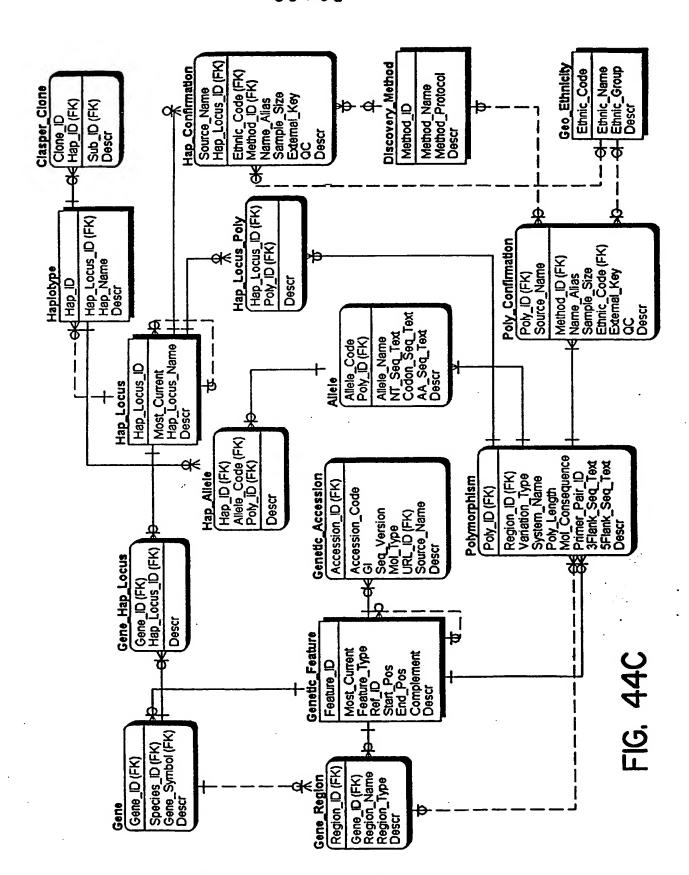


SUBSTITUTE SHEET (RULE 26)

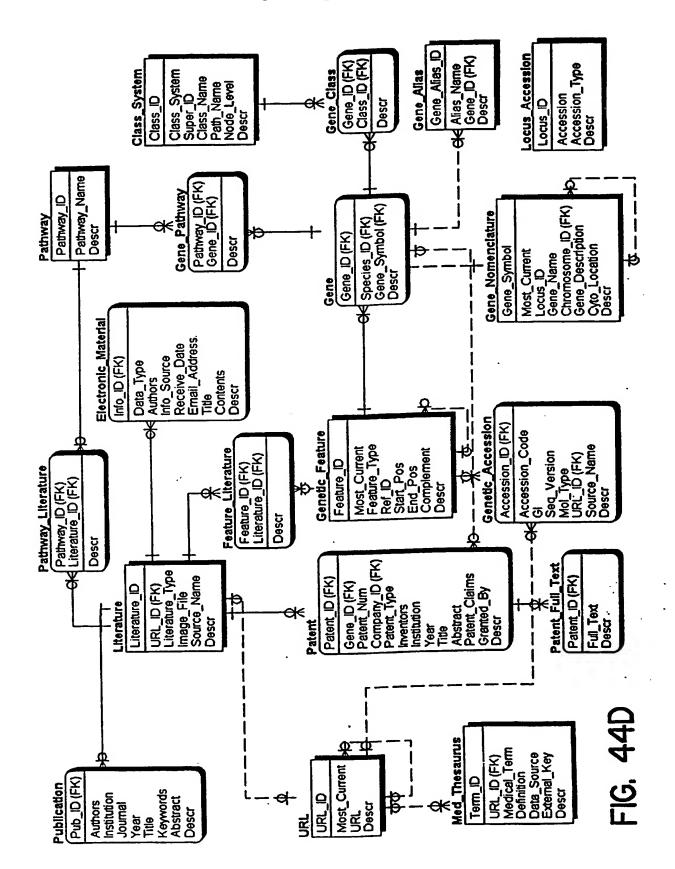


SUBSTITUTE SHEET (RULE 26)

55/62

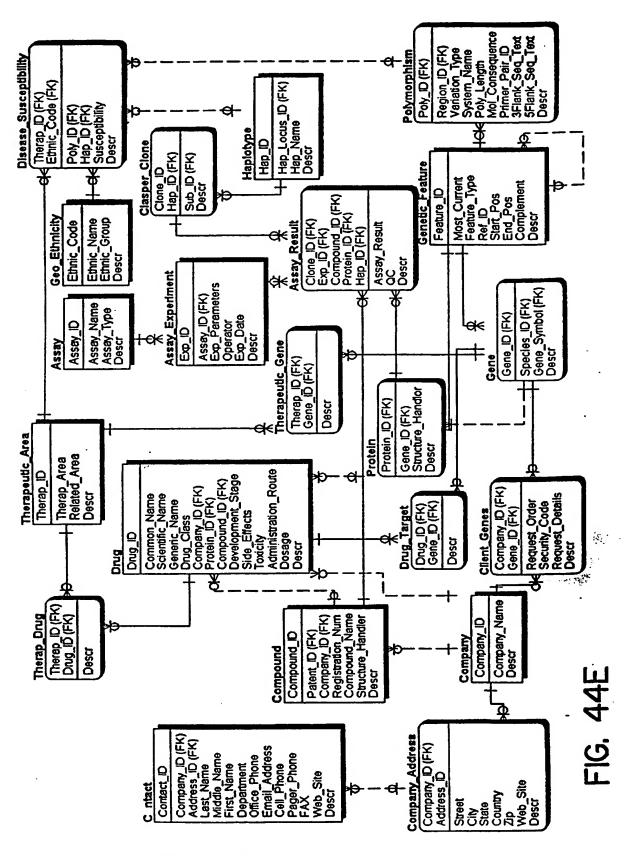


SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

57/62



SUBSTITUTE SHEET (RULE 26)

58 / 62

## Legend of Figures:



Rectangle Boxes: Tables in the database.

Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: | Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 8: \(\begin{align\*}
  ---\kappa \\
  \text{Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.}\)
- 10: | Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.

## FIG. 44F

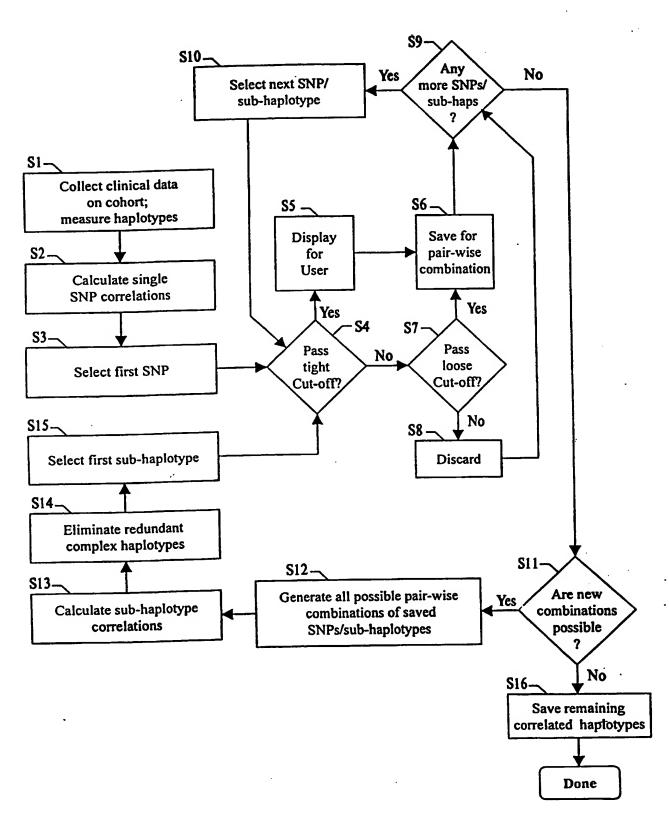


FIG. 45
SUBSTITUTE SHEET (RULE 26)

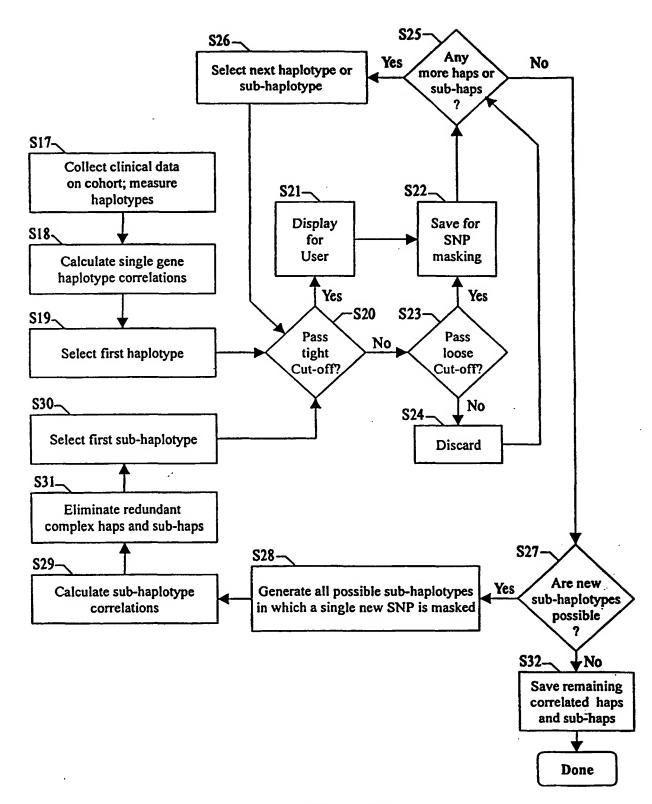


FIG. 46

**SUBSTITUTE SHEET (RULE 26)** 

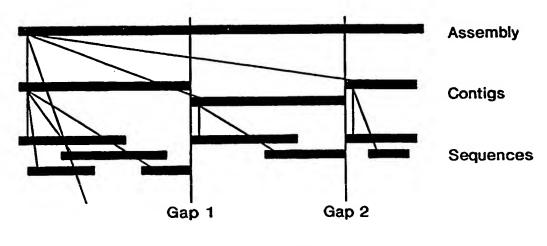


FIG. 47

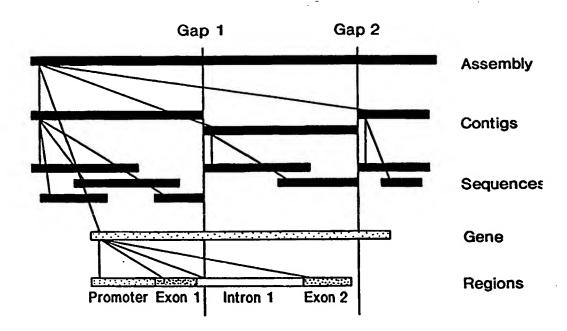


FIG. 48

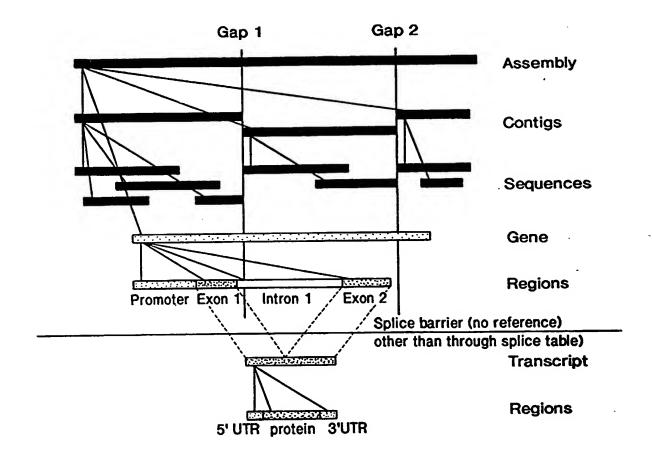


FIG. 49